
TASSEL: LD Pipeline: *Guide to using Tassel Pipeline*

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Prerequisites.....	1
Source Code.....	1
Install.....	1
Execute.....	1
Usage.....	2

Prerequisites

- Java SDK 5.0 or later (<http://java.sun.com/javase/downloads/index.jsp>).
- Tassel Standalone Build (http://www.maizegenetics.net/tassel/tassel2.1_standalone.zip)

Source Code

- <http://tassel.cvs.sourceforge.net/tassel/maizegenetics>

Install

Unzip the Tassel Standalone Build onto your file system. Change into the root directory:
tassel2.1_standalone.

Execute

On Windows, see `run_file_ld.bat` for an example how to execute the pipeline.

In Bash Shell, see `run_file_ld.pl` for an example how to execute the pipeline. If you are using a UNIX operating system, you may need to change the following line to use a `:` instead of a `;`.

```
my $CP = join(";", @fl);
```

Usage

```
java net.maizegenetics.pipeline.LDFileInputPipeline (-s <SNP file> | -p
<Poly file> | -a <Anno file>) [-gt Split|GenState|Dosage|OneGamete] [-if
png|gif|bmp|jpg|svg] [-of img|csv|tab] [-ldplotsize <num>] -o <output
file>
```

Must specify either -s, -p or -a	
-s <SNP file>	SNP data (Loads as sequence alignment)
-p <Poly file>	SNP data (Loads as polymorphism alignment)
-a <Anno file>	Load annotated alignment.
-gt <transform>	Optionally specify genotype transform if loading polymorphism alignment or annotated alignment
Split	Multiple alignments by gamete
GenState	Alignment based on genotypic state (e.g. A:a > Aa) (DEFAULT)
Dosage	Dosage state (additive & dominant)
OneGamete	One gametic alignment
-if <image format>	Optionally specify image format. Options: png (DEFAULT), gif, bmp, jpg, svg This only applies if output format is img
-of <output format>	Optionally specify output format. Options: img (DEFAULT), csv, tab
-ldplotsize <num>	Optionally specify LD plot size. Example: 1000 will produce 1000x1000 plot.
-ldplotlabels true false	Optionally specify whether to show the LD Plot labels. DEFAULT: true
-o <output file>	-o <output file>